

Figure 1: 121P1F1 SSH sequence of 254 nucleotides (SEQ ID: 1)

1 GATCACAGTC TTTGTATTTT TCTACTTCTG CCTTAGCTG TTCCCTTTGG TCTCGAAGTG
 5 61 AAGAAAAGTC TTTTGCTAGC CTGGTTCGCT CTTCGGTTTC ACATCGGGCA ATTTTAGCTT
 121 TCTCAATGCT TTTCTGTAGG CTTCATGCT TTTGACITCC CTCAGACAAC TGAGATTCCA
 181 GAACCTCCAA CTTATGTTTC CTTCATGAA GAGCTTTACT TGGAAAAGCC CAATATAAT
 241 TAGAAGTTCC GATC

Figure 2: The cDNA and Amino Acid Sequence(s)

Figure 2A. The cDNA (SEQ ID. NO. : 2) and amino acid sequence (SEQ ID. NO. : 3) of 121P1F1. The start methionine is underlined. The open reading frame extends from nucleic acid 82-699 including the stop codon.

1 ccaaaaatcaaaagcggtccggggcctgtccggcccccctctccccaagcgggggcccgccagc
 1 M S K K K G L S A E E K R
 61 ggaagcccccctgggcccggcgccATGTCAAGAGAAAAAGGACTGAGTGCAGAGAAAGAGAGA
 14 T R M M E I F S E T K D V F Q L K D L E
 121 ACTGGCATGATGGAATATTTTCTGAAACAAAAAGATGTATTTCAATTAAAAAGACTTGGAG
 34 K I A P K E K G I T A M S V K E V L Q S
 181 AAGATTGCTCCCAAGAGAAAAGGCATTACTGCTATGTTCAGTAAAAAGAGTCCTTCAAAGC
 54 L V D D S M V D D E E I G T S N Y Y W A
 241 TTAGTTTATCATGGTATGTTTACTGCGAGAGGATCGGAACCTTCAATPATIATTGGGCT
 74 F P S K A L R A R K R R L E V L E S Q L
 301 TTTCCAAGTAAAGCTCTTTATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAAGTTG
 94 S E S S Q K R A S D Q K S I E K A K I G
 361 TCTGAGGGAGTCAAAAGTATGCAAGCCTACAGAAAAGCATTGAGAAAAGCTAAAATTGGC
 114 R C E T E E R T R L A F E L S S L E D Q
 421 CGATGTGAAACGGAAGAGCGGAACCAAGGCTAGCAAAAGAGCTTTCTTCACTTGGAGACCAA
 134 R E Q L K A E V E K Y K D C D P Q V V E
 481 AGGGAACTAGCTAAAGGCAGAAAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAA
 154 E I F Q A N K V A K E A A N E W T D N I
 541 GAAATACGCCAAGCAAAATAAGTAGCCAAAGAAAGCTGCTAACAGATGGACTGATAACATA
 174 F A I K S W A K R K F G F E E N K I D E
 601 TTCGCAATAAAATCTTGGGCCAAAAGAAAAATTTGGGTTTGAAAGAAAATAAAATTGATAGA
 194 T F G I F E D F D Y I D *
 661 ACTTTTGGGAATTCCAGAAGACTTTGACTACATAGACTAAAatattccatgggtgggtgaagg
 721 atgtacaagcttggtgaatatgtaaattttaaacattatctaaactaagtgtactgaattg

781 tcgtttgcctgttaactgtgtttatcattttattaatgttaaataaaagtgtaaaaatgcaaa
841 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. : 4) and amino acid sequence (SEQ ID. NO. : 5) of 121PIF1 splice variant 1A. The start methionine is underlined. The open reading frame extends from nucleic acid 82-462 including the stop codon.

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5          1  ccaaaatcaaaagcgtccgggactgtccgcgcctctctcccaagcgcggggccgggcagc
      1          M S K F K G L S A E E K R
61 ggaagccctcgccgcgcgcgcATGTCAAAGAAAAAGGACTGAGTGCAGAAAGAAAGAGA
14 T R M M E I F S E T F D V F Q L K D L E
101 ACTGCGATGATGAAATATTTCTGAAACAAAGATGATTTCAATTAAAGACTTGGAG
10 34 K I A P K E K G I T A M S V K E V L Q S
131 AAGATTGCTCCCAAAAGAGAAAGGCAATTACTCTATGTCAGTAAAGAAAGTCTTCAAAGC
54 L V D D G M V D C E F I S T S N Y Y W A
241 TTASTTGATGATGGTATGTTGACTGTGAGAGGATCGGAACTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q D
15 301 TTCCCAAGTAAAGCTCTTTCATGCAAGGAAACATAAGGTTGAGCTTCTGSAATCTCAGGAC
94 P G C C F H E I I K V S Y Y F K F W L G
361 CCTGGCTGCTGCTCCCATGAAATAATTAAAGTCTCCCTATTATAGAAAAATCTGCTGCGC
114 A V A H A C N P S T L G G *
411 GCAGTGGCTCAAGCTGTGAATCCAGCACTTTGGGAGGCTGAGgcggggcagatcacgagg
20 441 tgaatttcccccaccccccacatgaagtgcaagatggagttgtctgaggggaagtcaaaagc
541 atgcaagcctacagaaaagcattgagaaagctaaaattggccgatgtgaaaagggaagagc
601 gaaccaggctagcaaaaagagctttcttccattcgagacccaaagggaacagctaaaggcag
661 aagtagaaaaatacaaaagactgtgatccgcaagttgtggaagaaatacgcacaagcaaaata
721 aagtagccaaagaagctgctaaacagatggactgataacatattcgcaataaaatcttggg
25 741 ccaaaagaaaatttgggtttgagaaaaataaaattgatagaaactcttggaattccagaag
841 actttgactacatagactaaaatattccatgggtgggtgaaggatgtacaagcttgtgaata
901 tgtaaattttaaaactattatctaactaagtgtactgaattgtogtttgcctgttaactgtg
961 tttatcatttttattaatgtttaataaagtgtaaaatgcacaaaaaaaaaaaaaaaaaaaaa
1021 aaaaaaaa
30

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Figure 2C. The cDNA (SEQ ID. NO. : 6) and amino acid sequence (SEQ ID. NO. : 1) of I21P1F1 splice variant 1B. The start methionine is underlined. The open reading frame extends from nucleic acid 501-860 including the stop codon.

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5      1  ccaaaatcaaaacgggtccgggacctgtcccgcacctctcccaagcgcggggccggccagc
      61  ggaagccacctggcgcgcgcacatgtcaaaqaaaaaaggagtgagtgccagaagaaaagaga
    101  actgcgatgatggaaatattttctgaaaacaaaagatgtattttcaattaaaagacttggag
    151  aagattgctcccaagagaaaaggaattactgtatgtcagtaaaaagaagtacctcaaaagc
    201  ttagttgatgatgggtatgggttgactgtgagaggatcgggaacttccaatttatatttgggt
    251  tttccaagtaaaagctcttcacgcaaggaaacataagttggagggtttctggaatctcaggac
    301  cctgggtgctgcttccatgaaataattaagctctctattatagaaaattctgggtgggt
    351  gcagtggttcacgcctgtaatccagcactctggggagggtgaggcgggcagatcacgagg
      1      M K C K M E L S E G S Q K H
    401  tgactttcccccaacccccacATGAAGTGCAGATGGASTTGTCTGAGGGAAGTCAAAAGC
    451  15  A S L Q K S I E K A K I G R C E T E E R
    501  ATGCAAGCCTACAGAAAAGCATTGAGAAAAGCTAAAATTGGCCGATGTGAAACGGAAGAGC
      35  T R L A K E L S S L R D Q R E Q L K A E
    601  GAACCAGGCTAGCAAAAGAGCTTTCTTCACTTTCGAGACCAAAGGGAACAGCTAAAGGCAG
      55  V E K Y K D C D P Q V V E E I R Q A N K
    651  AAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAAGAAATAACGCCAAGCAAATA
      75  V A K E A A N R W T D N I F A I K S W A
    701  AAGTAGCCAAAGAAAGCTGCTAACAGATGGACTGATAACATATTGCAATAAAATCTTGGG
      95  K R K F S F E E N K I D R T F G I P E D
    751  CCAAAAGAAAATTTGGGTTTGAAGAAAATAAAATTGATAGAACTTTTGGGAATTCCAGAAG
    801  25  F D Y I D *
    851  ACTTTGACTACATAGACTAAaataattccatgggtgggaaggatgtacaagcttgtgaata
    901  tgtaaatTTTTAAactatttatctaactaagtgtactgaactgtcgtttgcctgtaaactgtg
    951  tttatcatttttattaatgttaataaagtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaa
    1001  aaaaaaaa
    30

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Figure 2D. The cDNA (SEQ ID. NO. : 8) and amino acid sequence (SEQ ID. NO. : 9) of 121PIF1 splice variant 2. The start methionine is underlined. The open reading frame extends from nucleic acid 82-450 including the stop codon.

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5      1  ocaaaatcaaaagcggtccgggctgtccggtccctctccccaagcggggcccgccagc
      1      M S K K K G L S A E E K R
61  ggaagccccctgcgccccgcgccATGTCAAAGAAAAAAGGACTGAGTGCAGAAAGAAAAGAG
14  T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGAAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAACACTTGGAG
10  34  K I A P K E K S I T A M S V K E V L Q S
131 AAGATTGCTCCCAAAGAGAAAAGCATTACTGCTATGTCAGTAAAAAGAACTCCTTCAAAGC
54  L V D D G M V D C E E I G T S N Y Y W A
241 TTAGTTGATGATGSTATGGTTGACTGTGAGAGGATCGGAACTTCTAATTATTATIGGGCT
74  F P S K A L H A R K E K L E V L E S Q L
15  301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGSTTCTGGAATCTCAGTTG
94  S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAGTCAAAAACATGCAAGCCTACAGAAAAGCATTGAGAAAAGCTAAAATTGGC
114 F C E T A K Q I K *
421 CGATGTGAAACGGCCAAGCAAATAAAGTAGccaaaagaagctgctaacagatggactgata
20  481 acatattcgcaataaaaatcttgggccccaaaagaaaatttgggtttgaagaaaataaaattg
541 atagaacttttgggaattccagaagaactttgaactacatagactaaaatattccatgggtgg
601 gaaggatgtacaagcttgtgaatatgtaaatttttaaactattatctaactaagtgtactg
661 aattgtcggttgcctgtaaactgtgtttatcattttattaatgttaaataaagtgtaaaat
721 gcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

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25

Figure 2E. The cDNA (SEQ ID. NO. : 10) and amino acid sequence (SEQ ID. NO. : 11) of 121P1F1 splice variant 3. The start methionine is underlined. The open reading frame extends from nucleic acid 82-654 including the stop codon.

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5      1 ccaaaatcaaacycgctccgggcctgtcccgccccctctccccaagcgcgggcccgggccagc
      1      M S F K K G L S A E E F R
61 ggaagccccctgcgcgccgcgccATGTCAAAGAAAAAGGACTGAGTGCAGAAGAAAAGAGA
14 T R M M E I F S E T K I V F Q L K D L E
121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG
10 34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAATAAAAGAAGTCCTTCAAAGC
54 L V D D G M V D C E F I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAAGTCTAATTATTATGGGCT
74 F P S K A L H A R K H K L E V L E S Q L
15 301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAASTTGGAGGTTCTGGAATCTCAGTTG
94 S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAGTCAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC
114 F C E T E E R T F L A K E L S S L R D Q
401 CGATGTGAAACGGAAGAGCGAACCAGGCTAACAAGAGGCTTCTTCACTTCGAGAGCAA
20 134 E E Q L K A E V E K Y K E C D P Q V V E
481 AGGSAACAGCTAAAGGCAGAAAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGSA
154 E I H N I F A I K S W A K R K F G F E E
541 GAAATACATAACATATTGCAATAAAATCTTGCGCCAAAAGAAAATTTGGGTTTGAAGAA
174 N K I D R T F G I P E D F D Y I D *
25 601 AATAAAATTGATAGAACTTTTGAATTCCAGAAAGACTTTGACTACATAGACTAAaatatt
661 ccatggtggtgaaggatgtacaagcttggaatatgtaaatTTTAAactattatctaact
721 aagtgtactgaattgtcggttgctgtgaactgtgtttatcattttattaatgttaataaa
781 agtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

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Figure 2F. The cDNA (SEQ ID. NO. : 12) and amino acid sequence (SEQ ID. NO. : 13) of 121PIF1 splice variant 4. The start methionine is underlined. The open reading frame extends from nucleic acid 281-853 including the stop codon.

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5      1 gttttctgtattgtaatatgtagagcacattcagaaactgctcagtttcgaggttacctaa
      61 tggatcttcaactgtgtgccanttagtcgatttctgtgaaaaacgcccgggtttctgcccaaa
     121 gggcaggagtcgctctcttctgtgcccgggtgctcctgggttctgttagggcgctgttcttctt
     181 ttaaggacgctctcactgaatttaggcttctctgtgggttcctgatcatttaagtcctgtc
      1      M M E I F S E
     241 aaagaaaaaaggatcagagtgcagaaagaaaagagaaactcgcATGATGGAAATATTTTCTGA
     8      T K D V F Q L F D L E K I A F K E K G I
    301 AACAAAAGATGATATTTCAATTAAAAAGACTTGGAGAAGATTGCTCCCAAGAGAAAGGCAT
    28      T A M S V F E V L Q S L V D D G M V D C
    361 TACTGCTATTTAGTAAAAGAAATCTTTCAAAAGCTTAGTTGATGATGATGATGATGATG
    48      E F T G T S N Y Y W A F P S E A L H A F
    421 TGAGAGATTCGGAAGCTTCTAATTATATATGGGCTTTTCCAAATAAAGCTTCTTCATGCAAG
    68      K H K L E V L E S Q L S E G S Q K H A S
    481 GAAATATAAGTTGGAGSTTCTGGAATCTTCACTTGCTGAGGGAAGTAAAGCATGCAAG
    88      L Q K S I E F A F I G F D E T E E R T E
    541 CTACAGAAAAGCATTGAGAAAGCTAAATTTGGGCGATGTGAAACGGAAGAGGGAATCCAG
    108      L A K E L S S L R I Q R E Q L K A E V E
    601 GCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAAGGGGAATAGCTAAGGCAGAACTAGA
    128      K Y K D L D F Q V V E E I F Q A N K V A
    661 AAAATACAAAGACTGTGATCCGCAAGTTTGTGAAGAAATACGCCAAGCAATAAAGTACC
    148      E E A A N R W T D N I F A I K S W A F F
    721 CAAAGAAATGTCTAACAGATGGACTGATACATATTTGCAATAAATCTTGGGCCAAAG
    168      K F G T E E N K I D R T F S I F E E F I
    781 AAAATTTGGGTTTGAAGAAAAATAAATTGATAGAACITTTGGAATTCCAGAAAGATTTGA
    188      Y I D
    841 CTACATAGACTAAaattattccatggtggtggaaggatgtacaagcttgtgaatatgtaat
    901 tttaaaactattatctaactaaqgtgactgaattgtcgttttgcctgttaactgtgttatca
    961 ttttatttaagtcaaaataaagtgtaaaatggagatgttcttcaaccccttttggtaaaaca
    1021 aaagcaggatcataaacatatacccccagtggtcctcaaaaatagggaacttaaaaaatccat
    1081 ccattctcagccaaagtcgagcgccgcgaatttagtagtagtagcgccgctctajagga
    1141 tccaagcttcgtaacgggtgcatggaggtcctatagctcttctatagtgtaacctaattc
    1201 aagtt

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Figure 3:

Figure 3A. Amino acid sequence of 121PIF1 (SEQ ID. NO. : 14). The 121PIF1 protein has 205 amino acids.

1 MSKKKGLSAE EKRTRMMEIF SETKCVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
 61 DCEFIGTSNY YWAFPSKALH ARKHFLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETEEF
 121 TRLAKELSSL RLQREQLKAE VEKYFDCDPQ VVEEIRQANK VAKEAANRWT DNIFAIKSWA
 181 KRKEGFEEENK IDFTFGIPED FDYID

Figure 3B. Amino acid sequence of 121PIF1 splice variant 1A (SEQ ID. NO. : 15). The 121PIF1 splice variant 1A protein has 126 amino acids.

1 MSKKKGLSAE EKFTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDIGMV
 61 DCEFIGTSNY YWAFPSKALH ARKHKLEVLE SQDPGCCFHE IIKVSYRKF WLGAVAHACN
 121 PSTLGG

Figure 3C. Amino acid sequence of 121PIF1 splice variant 1B (SEQ ID. NO. : 16). The 121PIF1 splice variant 1B protein has 119 amino acids.

1 MKCKMELSEG EQKHASLQKS IEKAKIGRCE TEERTFLAKE LSSLRDQREQ LKAEVEKYKD
 61 CDPQVVEEIR QANKVAKEAA NRWTDNIFAI KSWAKEKFGF EENKIDRTFG IPEDFDYID

Figure 3D. Amino acid sequence of 121PIF1 splice variant 2 (SEQ ID. NO. : 17). The 121PIF1 splice variant 2 protein has 122 amino acids.

1 MSKKKGLSAE EKRTRMMEIF SETKDVFQIK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
61 DCERIGTSNY YWAFFSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETAKQ
121 IK

Figure 3E. Amino acid sequence of 121P1F1 splice variant 3 (SEQ ID. NO. : 18). The 121P1F1 splice variant 3 protein has 190 amino acids.

5 1 MSKKKGLSAE EKRTPMMEIF SETEDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDLGMV
 61 DCERIGTSNY YWAFFSFALH ARKHFLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETEER
 121 TRLAKELSSL RDQREQLKAE VEKYEDCDPQ VVEEIHNIFA IKSWAKFKFG FEENKILRTF
 181 GIPEDFDYIL

10

Figure 3F. Amino acid sequence of 121P1F1 splice variant 4 (SEQ ID. NO. : 19). The 121P1F1 splice variant 4 protein has 190 amino acids.

15 1 MMEIFSETKI VFQKLDLEKI AFKEKGITAM SVKEVLQSLV DDGMVDCEFI GTSIIYYWAFP
 61 SKALHAFKHF LEVLESQISE GSQKHASLQK SIEKAKIGRC ETEERTFLAK ELSSLRDQRE
 121 QLKAEVEKYK DCDPQVVEEI RQANKVAKEA ANRWTDNIFA IKSWAKFKFG FEENKIDETF
 181 GIPEDFDYID

Figure 4A

Amino Acid Alignments.

5 Alignment of 121P1F1 protein and its variants.

A) CLUSTAL W alignment of 121P1F1 and variants 1-3. (SI Q ID Nos 3, 5, 7, 9 and 11)

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10 121P1F01 -----MSKKKGLSAAEEKPTPMMEIFSETFDVFQLFDLEKIAPKEFGITAMSVKE
    sv1A -----MSKFFFGLSAEEKPTFMMEIFSETFDVFQLFDLEKIAPKEFGITAMSVKE
    sv1B -----MKCFMELSEGSQFHASLQKSIKFAFIQFCETEEFTLAKELSSSLFDQFE
    sv-1 -----MSKFFFGLSAEEKPTFMMEIFSETFDVFQLFDLEKIAPKEFGITAMSVKE
    sv-3 -----MSKFFFGLSAEEKPTFMMEIFSETFDVFQLFDLEKIAPKEFGITAMSVKE

15 121P1F01 VLQSLVLDGMVDCEFIIGTSNYYWAFISFALHAPFFHFLEVLESQQLSEGSQF-HASLQKS-I
    sv1A VLQSLVLDGMVDCEFIIGTSNYYWAFISFALHAPFFHFLEVLESQDI-GCCF-HEIIFVSYY
    sv1B QLFAEVEF-YKDCIH QVVEHIRQANFVAKEAANFWDNI FAIFSWAKRFFFGFEENFID--
    sv-1 VLQSLVLDGMVDCEFIIGTSNYYWAFISFALHAPFFHFLEVLESQQLSEGSQF-HASLQKS-I
    sv-3 VLQSLVLDGMVDCEFIIGTSNYYWAFISFALHAPFFHFLEVLESQQLSEGSQF-HASLQKS-I

20 121P1F01 EFAFIQFCETEEFTLAKELSSSLFDQREQLKAEVVEFYHDCDPQVVEEIFQANKVAEEAAN
    sv1A FFFWLGAFAHACNPSTLGG-----
    sv1B FTFGIPEDFDYID-----
    sv-1 EFAFIQFCETAKQIF-----
    sv-3 EFAFIQFCETEEFTLAKELSSSLFDQREQLKAEVVEFYHDCDPQVVEEIHNI FAIKSWAKR

30 121P1F01 FWTDNIFAIKSWAKRKFGFEENKIDFTFGIPEDFDYID
    sv1A -----
    sv1B -----
    sv-1 -----
    sv-3 FFGFEENKIDRTFGIPEDFDYID-----

35

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Figure 4B

Clustal alignment of 121P1F1 and variants 1A and 4 (SI Q ID Nos 3, 13 and 5)

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40 1 121P1F01 MSKKKGLSAAEEKPTPMMEIFSETFDVFQLFDLEKIAPKEFGITAMSVKEVLQSLVLDGMVDCEFIIGTSNYYWAFISFALHAPFFHFLEVLESQQLSEGSQF-HASLQKS-I
    2 sv-4 -----MSKFFFGLSAEEKPTFMMEIFSETFDVFQLFDLEKIAPKEFGITAMSVKEVLQSLVLDGMVDCEFIIGTSNYYWAFISFALHAPFFHFLEVLESQDI-GCCF-HEIIFVSYY
    3 sv-1A MSKKKGLSAAEEKPTPMMEIFSETFDVFQLFDLEKIAPKEFGITAMSVKEVLQSLVLDGMVDCEFIIGTSNYYWAFISFALHAPFFHFLEVLESQQLSEGSQF-HASLQKS-I

45 1 121P1F01 QQLSEGSQFHASLQKSIKFAFIQFCETEEFTLAKELSSSLFDQREQLKAEVVEFYHDCDPQVVEEIFQANKVAEEAANFFFWLGAFAHACNPSTLGG-----
    2 sv-4 QQLSEGSQKHAIAKQIEKAKTIRKCTEER TELAKFIINAIQRE IIRAKVEER TELQI IVEEIRQVANKVAKRA ANKWTNIFAIKWA
    3 sv-1A QQLSEGSQFHASLQKSIKFAFIQFCETEEFTLAKELSSSLFDQREQLKAEVVEFYHDCDPQVVEEIFQANKVAEEAANFFFWLGAFAHACNPSTLGG-----

50 1 121P1F01 KKKFGFEENKIDRTFGIPEDFDYID
    2 sv-4 KKKFGFEENKIDRTFGIPEDFDYID
    3 sv-1A -----

55

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Figure 4C

C) Alignment of LTP1 and variant (SEQ ID NO 20) Alignment with human GAJ (SEQ ID NO 21)

Identities = 205/205 (100%), Positives = 205/205 (100%)

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121P1: 1  MSFFFGLSAEEFFTFMMEIFSETKDVFCQKDLKLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60
      MSFFFGLSAEEFFTFMMEIFSETKDVFCQKDLKLEKIAPKEKGITAMSVFEVLQSLVDDGMV
10  Sbjct: 1  MSFFFGLSAEEFFTFMMEIFSETKDVFCQKDLKLEKIAPKEKGITAMSVFEVLQSLVDDGMV 60

121P1: 61  DCEFIIGTSNYYWAFPSFALHAFHHFLEVLESQLESGSQKHASLQKSIKFAFIIGPCETEEF 120
      DCEFIIGTSNYYWAFPSFALHAFHHFLEVLESQLESGSQKHASLQKSIKFAFIIGPCETEEF
15  Sbjct: 61  DCEFIIGTSNYYWAFPSFALHAFHHFLEVLESQLESGSQKHASLQKSIKFAFIIGPCETEEF 120

121P1: 121 TFLAKELSSLFQFEQLKAEVEFYFDCEPQVVEEIFQANKVAKEAANFWTDNIFAISWA 180
      TFLAKELSSLFQFEQLKAEVEFYFDCEPQVVEEIFQANKVAKEAANFWTDNIFAISWA
20  Sbjct: 121 TFLAKELSSLFQFEQLKAEVEFYFDCEPQVVEEIFQANKVAKEAANFWTDNIFAISWA 180

121P1: 181 KKKFGFEENKIDFTFGIPEDFDYID 205
      KKKFGFEENKIDFTFGIPEDFDYID
20  Sbjct: 181 KKKFGFEENKIDFTFGIPEDFDYID 205

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Figure 4D

D) Alignment of 121P1 and variant (SEQ ID NO 22) with closest mouse homolog, a hypothetical 24.2 KDa protein. (SEQ ID NO 23)

5 Identities = 183/205 (89%), Positives = 193/205 (93%)

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121P1: 1  MSKKKGLSALEKKRTRMMEIFSETKDVVFQLKLEKFLAPKEKGITAMSVKEVLQSLVDDGMV 60
      MSKK+GLS EEKTRTRMMEIF ETKDVVFQLKLEK+APKEKGITAMSVKEVLQSLVDDGMV
Sbjct: 1  MEKKEGLSGEEKRTRMMEIFFETKDVVFQLKLEKFLAPKEKGITAMSVKEVLQSLVDDGMV 60

10 121P1: 61  DCERIGTSNYYWAFPSKALHAPFKHLEVLSQLSEGSQKHASLQKSIEKAKIGRCETEER 120
      DCERIGTSNYYWAFPSKALHAPK KLE L SQLSEGSQKHA LQKSIEKA++GR ETEER
Sbjct: 61  DCERIGTSNYYWAFPSKALHAPFKLEALNSQLSEGSQKHADLQKSIEKARVGRQETEER 120

15 121P1: 121 TFLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANFWDNIFAISWA 180
      LAHEL S FDDR+QLKAEVEKY++CDPQVVEEIR+ANKVAKEAANFWDNIFAISWA
Sbjct: 121 AMLAKELFSFEDQROQLKAEVEKYRECDPQVVEEIREANKVAKEAANFWDNIFAISWA 180

20 121P1: 181 FEFKFGFEENKIDFTFSIPEDFDYID 205
      FEFKFGFEE+KID+ FGIPEDFDYID
Sbjct: 181 FEFKFGFEESHIDENFGIPEDFDYID 205

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Figure 4E

E. Alignment of 121PHE and variant (SLQ ID NO: 243)

with>gi.1175412|sp|QC9739|YA53_SCHFO HYPOTHETICAL 24.2 KD PROTEIN
 C13A11.03 IN CHROMOSOME I :

gi|7490680|pir|J137610 hypothetical coiled-coil protein - fission yeast
 (Schizosaccharomyces pombe)

gi|984224|er|CAA90804.1 (Z54096) hypothetical coiled-coil protein
 [Schizosaccharomyces pombe]

Length = 110

Score = 121 bits (305), Expect = 5e-27

Identities = 81/202 (40%), Positives = 115/202 (56%), Gaps = 6/202 (2%)

Query: 5 KGLSAEEKKFTFMMEIFSETHDVFQLEFDLEKIAAPKEKGITAMSVKEVLQSLVDDGMVDCER 64
 KGLS EEF F+ IF ++KD FQLK++EK+ K K I +VK+VLQSLVDD +V E+
 Sbjct: 4 KGLSLAEKFRFELEAIFHDSKDFQLKEVEKLGSK-KQIVLQTVKDVLQSLVDDNIVKTEK 62

Query: 65 IGTSNTYWWAFPSKALHAKKHKLEVLLESQLESGSQKHASLQKSIEKAKIGR----CETEEF 120
 IGTSNTYW+PES A +F+ L L++QL + QK +L ++I K R E +
 Sbjct: 63 IGTSNTYWSFESDAKRSKESVLGSLQAQLDDLKQKSKTLDENISFEKSKREDNEGTENDAN 122

Query: 121 TPLAKELSSLFQREQLKAEVEKYKICDPQVVVEEIRQANKVAKEAANFWTDNIFAISWA 180
 + L + + + LK ++ Q+P+ E + K EAAN WTD I + ++

Sbjct: 123 QYTLELLHAKESSELKLLKTQLSNINHCNPETFELKNENTKKYMEAAANLWTDQIHTLIAFC 182

Query: 181 KFKFGFEENKIDETFGIPEDFD L02
 F G + N+I IPED D

Sbjct: 183 -FDMGADTNQIREYCSIPEDLD L03